

GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: December 15, 2003, 14:50:12 ; Search time 21 Seconds

(without alignments)
1419.633 Million cell updates/sec

Title: US-09-831-805A-6

Perfect score: 1635

Sequence: 1 MALRRPRLRLCARLPDFLL.....VNYIRTDDEGDPFRHKSFEVI 310

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : PIR 76:*

1: pirl:*

2: pirl:*

3: pirl:*

4: pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	419	25.6	299	2 S56749	junctional adhesio
2	187	11.4	725	2 JE0099	neural cell adhesi
3	186	11.4	1088	1 IJX1ML	neural cell adhesi
4	180.5	11.0	1894	2 C54689	protein-tyrosine-p
5	180	11.0	333	2 A31923	amalgam protein pr
6	177	10.8	725	2 JE0100	neural cell adhesi
7	177	10.8	1092	1 JN0635	neural cell adhesi
8	171.5	10.5	725	1 IJMSNG	neural cell adhesi
9	171.5	10.5	1115	1 IJMSNL	neural cell adhesi
10	170.5	10.4	858	1 IJRTNC	neural cell adhesi
11	169.5	10.4	1912	2 A56178	protein-tyrosine-p
12	164.5	10.1	1051	2 A39712	kinase-like protei
13	164.5	10.1	3707	2 S18352	heparan sulfate pr
14	163.5	10.0	853	1 JUBONG	neural cell adhesi
15	162.5	9.9	6642	2 T29757	protein UNC-89 - C
16	161.5	9.9	1612	2 T30805	ductal protein - hu
17	161	9.8	7962	2 I38346	elastic titin - hu
18	159.5	9.8	1033	2 S19247	cell adhesion prot
19	159	9.7	358	2 UC2457	vascular cell adhe
20	159	9.7	1323	2 PN0568	connectin 3B - chn
21	159	9.7	4162	2 T42633	connectin/titin -
22	157	9.6	1907	2 S50893	protein-tyrosine-p
23	156	9.5	1091	1 IJCHNL	neural cell adhesi
24	156	9.5	1501	2 S46217	protein-tyrosine-p
25	156	9.5	1863	2 S46217	protein-tyrosine-p
26	155.5	9.5	761	1 IJHONG	neural cell adhesi
27	155.5	9.5	1259	2 A43425	Bravo/Nr-CAM cell
28	155.5	9.5	1268	1 A39640	neural cell adhesi
29	154.5	9.4	495	2 T25750	hypothetical prote

30	153.5	9.4	365	2 JC7780	coxackie- and ade
31	153	9.4	352	2 T33433	hypothetical prote
32	153	9.4	875	2 T33434	hypothetical prote
33	152	9.3	483	2 T17346	hypothetical prote
34	151	9.2	1651	2 T14160	transmembrane rece
35	150.5	9.2	702	2 A36319	carcinoembryonic a
36	150	9.2	1262	1 B48758	protein-tyrosine-p
37	150	9.2	1496	1 A48758	protein-tyrosine-p
38	149.5	9.1	1897	1 TDHULK	leukocyte antigen-
39	149	9.1	521	2 S34338	leukocyte antigen-
40	149	9.1	1898	2 S46216	leukocyte antigen-
41	148.5	9.1	646	2 T38049	cell surface glyco
42	148.5	9.0	871	1 A48696	protein-tyrosine k
43	147.5	9.0	881	1 A48697	protein-tyrosine k
44	147	9.0	338	2 JC5519	50K glycoprotein p
45	147	9.0	344	2 I56551	neurotrophin - rat

ALIGNMENTS

RESULT 1

junctional adhesion molecule precursor - human
N.Alternate names: F11 platelet antigen; platelet adhesion molecule PAM-1; platelet F11
C.Species: Homo sapiens (man)
C.Date: 27-Oct-1995 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C.Accession: A59406; S56749
R.Ozaki, H.; Ishii, K.; Horuchi, H.; Arai, H.; Kawamoto, T.; Okawa, K.; Iwamatsu, A.; K
J. Immunol. 163, 553-557, 1999
A.Title: Cutting edge: combined treatment of TNF-alpha and IFN-gamma causes redistributi
A.Reference number: A59406; MUID:99323940; PMID:10395639
A.Accession: A59406
A>Status: preliminary
A.Molecule type: DNA
A.Residues: 1-299 <OZA>
A.Cross-references: GB:AAD42050; NID:95326797; PIDN:AAD42050.1
R.Naik, U.P.; Ehrlich, Y.H.; Kornecki, E.
Biochem. J. 310, 155-162, 1995
A.Title: Mechanisms of platelet activation by a stimulatory antibody: cross-linking of a
A.Reference number: S56749; MUID:95374438; PMID:7646439
A.Accession: S56749
A.Molecule type: protein
A.Residues: 28-49; 'X', '51-53-62-73', 'E', '75-103-123', 'F', '125-130', 'FDRDXIRLYNXY', 'LT', '206', 'X'
A.Note: the order of the peptides other than the amino terminus was not determined
C.Genetics:
A.Gene: JAM
C.Keywords: glycoprotein; phosphoprotein; platelet aggregation; platelet membran
F.1-25/Domains: signal sequence #status predicted <SIG>
F.26-29/Product: junctional adhesion molecule #status predicted <MAT>

Query Match	25.6%	Score 419;	DB 2;	Length 299;
Best Local Similarity	32.8%	Pred. No. 3e-27;		
Matches	101;	Conservative	47;	Mismatches 138; Indels 22; Gaps 7;
QY	8	RRLRCARLPDFLLPFGCLIGAVNLKSNRTPVQVFESEVELSCITTSQSDPRLEW	67	
DB	9	RRLCLL-----FLIALISLALGSLVTVNHSSEPVRIENNPKSCAR--SGFSPRLEW	62	
QY	68	KKIODEQTVVFFDNKIOGDLGRAELIGKTSLKIMVTRDSALYRCEVVARNDREKD	127	
DB	63	KDQGDTRRLVGVNKNKIFASVEDRVTFL-PTGITFKSVTRDGTGYTC-MWSEEGNSYG	120	
QY	128	ELVIELTVQVKEVTVVVCRAVPVGNKATLHCQSEBHPRHYSWYNDVLPRTDSKAN	187	
DB	121	EKKVILTVLVPSEKPTVNI-PSATIGNRAVLTCSDQSPPEEYVTFKGVMPNPKST	180	
QY	188	PPFRSSSHLNSGTLVFAVHKDSCGYCIAINDGSARCEQO-EMEVYDLNIGGII	246	
DB	181	RAFSNSVYLVNPTTLELFDPLSASDTGEGSEANGTGTPMSTNAVMEAVERVGVIV	240	
QY	247	GGVLVLAVALITLIGICCAVRRGYFINNKQDGS---YKNPKGPDGVNYYIRTDDEQDF	302	

F11542/Binding site: substrate phosphate (Arg) #status predicted
F11826/Active site: Cys (phosphocysteine intermediate) #status predicted
F11832/Binding site: substrate phosphate (Arg) #status predicted

Query Match 11.0%; Score 180.5; DB 2; Length 1894;

Best Local Similarity 28.8%; Pred. No. 1.7e-06;
Matches 72; Conservative 34; Mismatches 75; Indels 69; Gaps 15;

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QY 3 LRRPRLRL-----CARLPDFLLLPFGCLIGAVNLKSSRTYVVOEFSEVELSCIT 56
DB 11 VRRPILSLTLFLPLCAETPRPF-----TRTVDTQTVSGVASTFC 52
QY 57 DSQTS DPR--IEW-----KKIQDEQTTTFYFNDKIQGLAGRAELIKTSLKIMWTRRDS 110
DB 53 QA-TDDPRKIVWKKKKVSNQREVEIEFD-----GSGSVLRIQPLR-----TPRDE 100
QY 111 ALYREVVANRDKRIDELIVELTVQKVPYVCKAVPKAVPKM-----ATL 158
DB 101 AIYEC--VASNNVGBI--SVSTRLTIVLRBD-----QIPRPFPTIDMGPOLVKVERTRTATM 152
QY 159 HQESEGHPHRYSWYRNDVPLPTDSRANPRFRNSSHNSSET-GTIVFTAVHKDSDGY 217
DB 153 LCAAS-GNPDEPITTFKDFLPVDI-SNNNGRIK---QIRSESIGALQIEGSESDQGY 206
QY 218 YCIASNDGS 227
DB 207 ECVATNSAGT 216

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RESULT 5

A11923
amalgam protein precursor - fruit fly (*Drosophila melanogaster*)

C/Species: *Drosophila melanogaster*
C/Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 21-Jul-2000
C/Accession: A11923
R/Seeger, M.A.; Halfley, L.; Kaufman, T.C.
Cell 55, 589-600, 1988
A/Title: Characterization of amalgam: a member of the immunoglobulin superfamily from *D. A. Reference number: A11923; MUID:89028670; PMID:3141062*
A/Accession: A11923
A/Molecule type: DNA
A/Residues: 1-333 <SEB>
A/Cross-references: GB:M23561; NID:G156920; PIDN:AAA28367.1; PID:G156921
C/Genetics:
A/Gene: FlyBase:ama
A/Cross-references: FlyBase:FBgn0000071

Query Match 11.0%; Score 180; DB 2; Length 333;
Best Local Similarity 26.8%; Pred. No. 2.3e-07;
Matches 52; Conservative 39; Mismatches 83; Indels 20; Gaps 5;

```

QY 35 KSSNTPVVOEFSEVELSCITDSDPRIEWKKIQDEQTTTFYFNDKIQGLAGRAEI 94
DB 143 EMTPTKSTLTVECONELTC--HANGFPKPTISMAR-----EHNAMPAGGHL 187
QY 95 LKTSIKIMWTRRDSALRCCEVANDKKEIDELIVELTVQKVPYVCKAVPKAVPK 154
DB 188 LAEPTLRISVHRMDRGTYC--IAONGEGQPKRILREVERPPIAQRKIAOWSH 245
QY 155 MATLHQESEGHPHRYSWYRNDVPLPTDSRANPRFRNSSHNSSETGTLVFTAVHKDS 214
DB 246 SAELER-SVQGYRPAITVWVKNGVPL--QSSRHHEVANANASSGTTTSLRLDSGDEDF 302
QY 215 GQYICIASNDGSA 228
DB 303 GDYICNATKLGHA 316

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RESULT 6

JE0100
neural cell adhesion molecule 2 - African clawed frog

N/Alternate names: N-CAM 2
C/Species: *Xenopus laevis* (African clawed frog)

C/Date: 19-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C/Accession: JE0100
R/Kudo, M.; Takayama, E.; Tadokuma, T.; Shiohawa, K.
Biochem. Biophys. Res. Commun. 245, 127-132, 1998

A/Title: Molecular cloning of *sed*-form neural cell adhesion molecules (N-CAMs) as the ma
A/Reference number: JE0099; MUID:98204770; PMID:9535795
A/Accession: JE0100
A/Molecule type: mRNA
A/Residues: 1-725 <KUD>
A/Cross-references: DDBJ:AB008163; NID:G3116228; PIDN:BA25932.1; PID:G3116229

A/Experimental source: heart
C/Comment: This protein mediates and regulates various cell-cell interactions through bc
C/Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
F/413-475/Domain: immunoglobulin homology <IMM>
F/512-589/Domain: fibronectin type III repeat homology <3PR>

Query Match 10.8%; Score 177; DB 2; Length 725;

Best Local Similarity 29.5%; Pred. No. 1.1e-06;
Matches 62; Conservative 28; Mismatches 86; Indels 34; Gaps 11;

```

QY 30 GAVNLKSSNR-----TPVVOEFSEVELSCITDSDSDPR-IEWK-KIQDEQTTVFYFND 82
DB 105 GTVNLKITYQKLTFRKAPPPQETBEEDVILICDVSSISITIMHKKGD-----VIRK 159
QY 83 KIQGLAGRAELIKTSLKIMWTRRDSALYRC--VVARNDKKEIDELIVELTVQKVPY 140
DB 160 DV-----RFVVLANNVLIQIRIGIKKTDEGNRCERILARG---EINVKDIQIVNVPL 210
QY 141 TPV--CRVPKAVPKVKAATLHQESEGHPHRYSWYRNDVPLPTDSRANPRFRNSSHIN 198
DB 211 IQARQIRVNAVATAMDESIVLSC-DADGFPDEISWLKGEPI-EDGEERKISF-----N 261
QY 199 SETGLVFTAVHKDSDGYICIASNDGSA 228
DB 262 EDKSEMTIYRVEKDEAEYSCLANNQGEA 291

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RESULT 7

JN0635
neural cell adhesion molecule 2 precursor - African clawed frog

C/Species: *Xenopus laevis* (African clawed frog)
C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 22-Jun-1999
C/Accession: JN0635
R/Tonissen, K.F.; Krieg, P.A.
Gene 127, 243-247, 1993
A/Title: Two neural-cell adhesion molecule (NCAM)-encoding genes in *Xenopus laevis* are ex
A/Reference number: JN0635; MUID:93273239; PMID:7684721
A/Accession: JN0635
A/Molecule type: mRNA
A/Residues: 1-1092 <TON>
A/Cross-references: GB:M76710; NID:G214611; PIDN:AAA49910.1; PID:G214612
C/Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
C/Genetics:
A/Gene: NCAM2

C/Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C/Keywords: alternative splicing; cell adhesion; duplication; heparin binding; siologlyc
F/1-19/Domain: signal sequence #status predicted <SIG>
F/120-1092/Product: neural cell adhesion molecule 2 #status predicted <EXT>
F/34-95/Domain: extracellular #status predicted <EXT>
F/129-188/Domain: immunoglobulin homology <IMM2>
F/149-153/Region: heparin binding #status predicted
F/158-162/Region: heparin binding #status predicted
F/317-381/Domain: immunoglobulin homology <IMM3>
F/413-475/Domain: immunoglobulin homology <IMM4>
F/512-589/Domain: fibronectin type III repeat homology <FN3A>
F/619-680/Domain: fibronectin type III repeat homology <FN3B>
F/706-723/Domain: transmembrane #status predicted <TM>
F/724-1092/Domain: intracellular #status predicted <INT>
F/41-93,136-186,232-282,323-379,420-473/Disulfide bonds: #status predicted
F/219,310,341,417,443,472/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 10.8%; Score 177; DB 1; Length 1092;

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